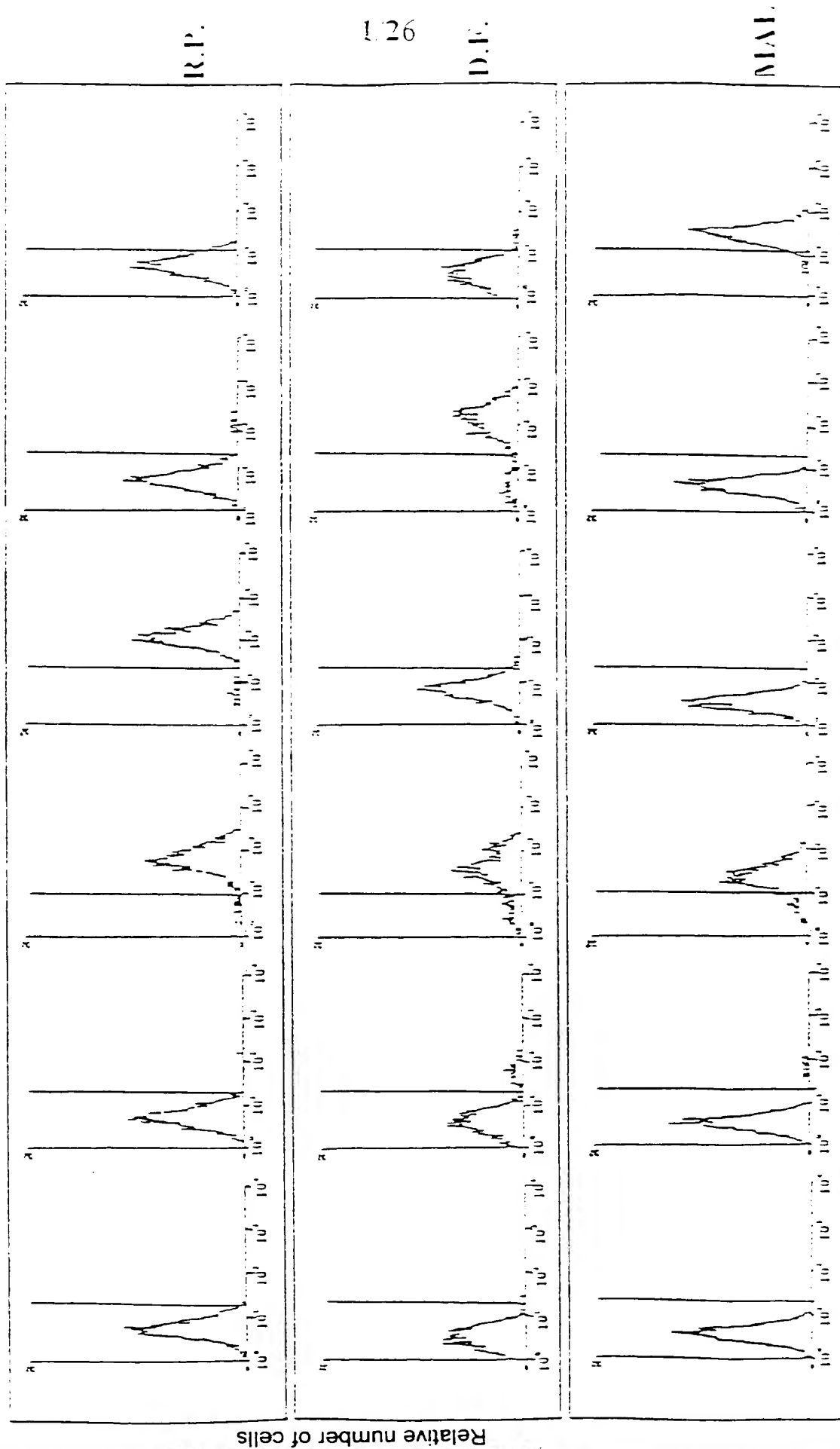


C anti-CD3 anti-CD16 anti-CD158 anti-CD158 anti-CD158  
 (p50.1, EB6) (p50.2, GL183) (p50.3, PAN250)

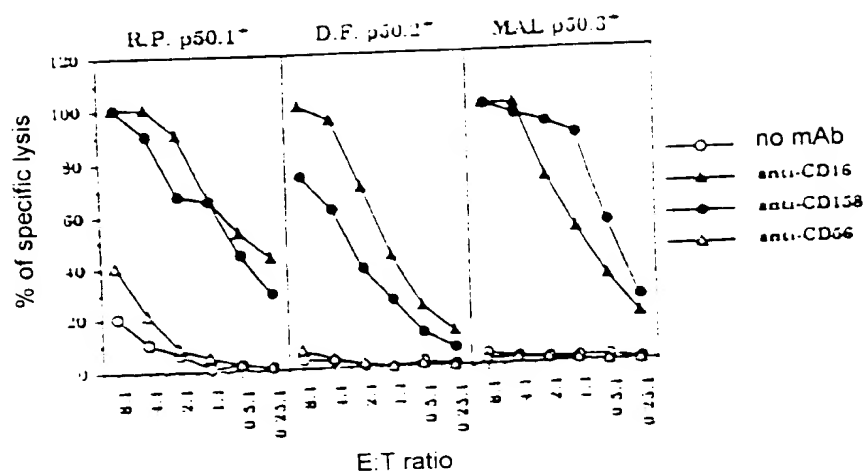


Intensity of fluorescence

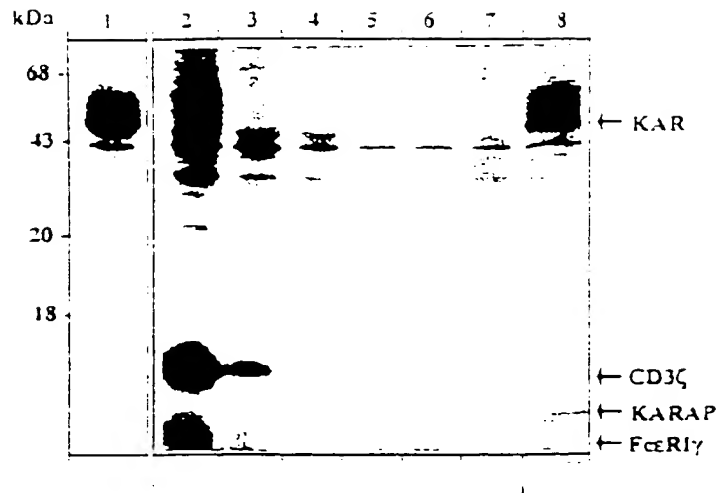
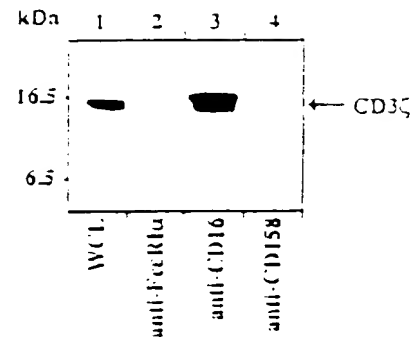
Figure 1A

2.26

Figure 1B



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Figure 2AFigure 2B

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Figure 3A

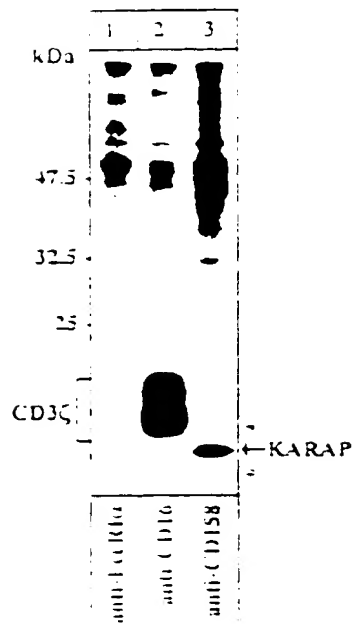


Figure 3B

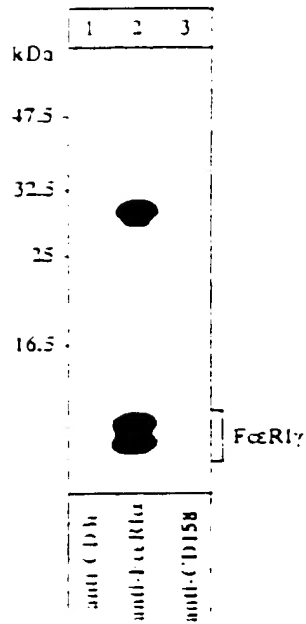
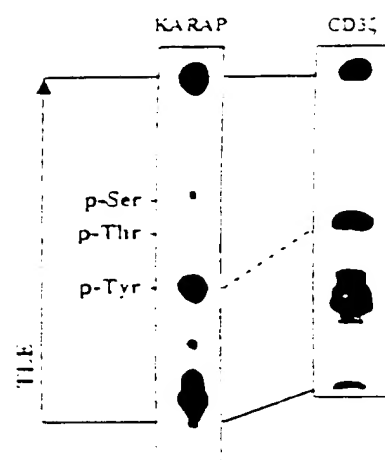
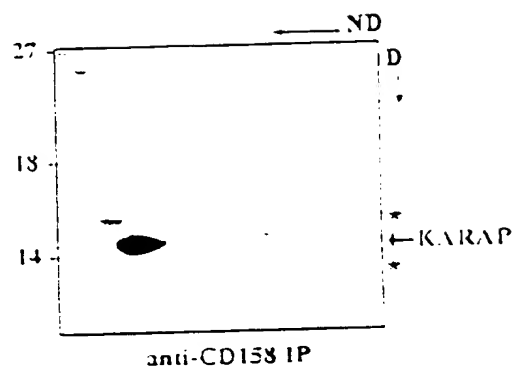


Figure 3C

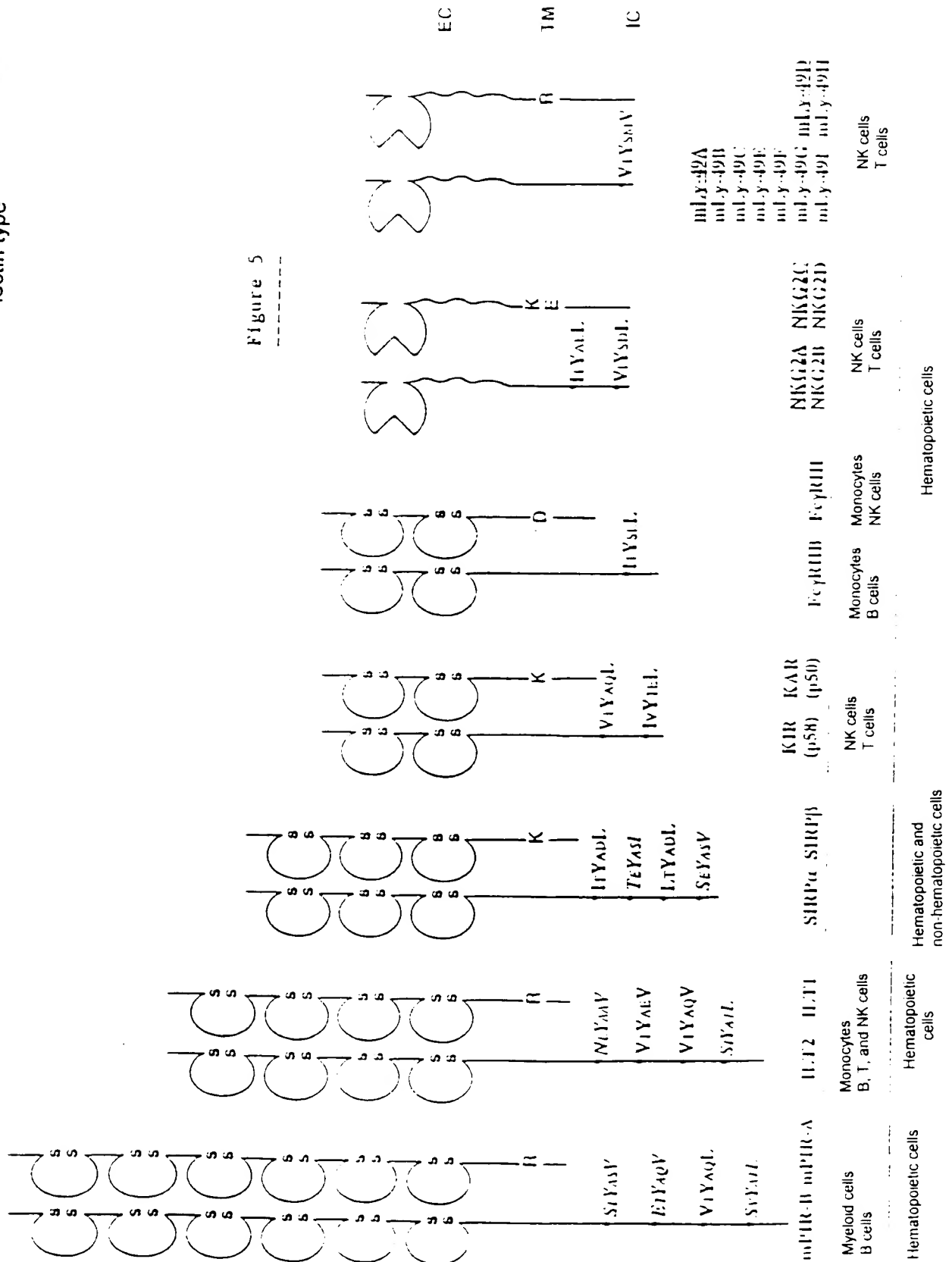


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Figure 4

lectin type

Figure 5



# NK p58/50 cell receptors for class I MHC molecules

Figure 6

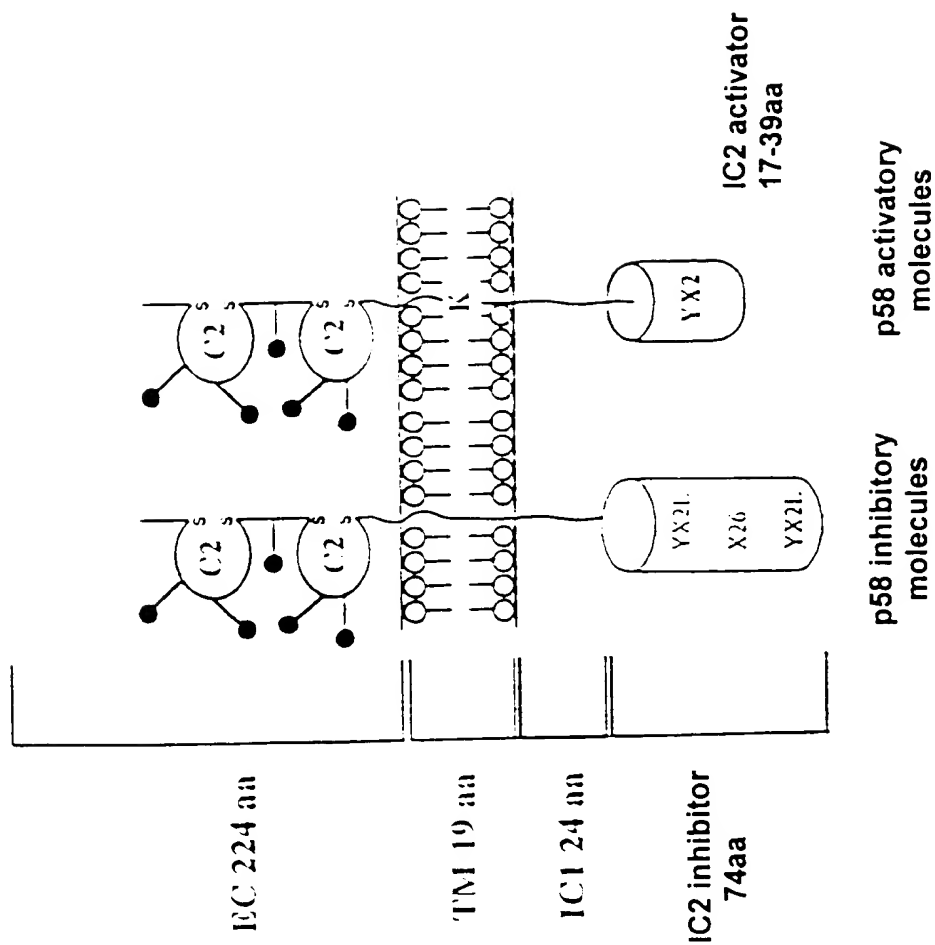


Figure 7

1 ggtaacacaa ggtccacaa gccctggac tgggtgtcc agtgcatac tggccacaa  
61 ggggtctgg agctctgg tgcctgt tctctgt cctctgact gtgggaggat  
121 taagtccgt acaggccag agtgacac tccaagatg cgaatgtct tccgtgagcc  
181 ctggtgact gtctgggaa gttctgggt acgtgtgt gactctgtg atgcccgg  
241 ctgtgactc tctggccgc ctggtctcc gaggtaagg gacagcggaa gggaccggg  
301 aacaacacat tctgagact ggtctgct atcaggagct tcagggtcag agacatgaag  
361 tatacgtga cttcaacaa caggggcaat attacagatg agcccactct atgccatca  
421 ggggtctgat gccaggatcc ggtcaaca gatgctact caacaagccc tctctgagat  
481 caggactccc gttgaatac agatccacag ggtact



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Figure 3

1/1

cag agt gac acc ttc cca aga tgc gac tgt tcc tcc gtc agc ccc ggt gta cct tcc ggt  
 Q S D T F P R C C C S S V S P G V L S G

31/11

61/21

31/31

att gtt cct ggt gac ttc gtc ttc acc cct cct att gcc cct gct gtc ttc tcc cct ggt  
 I V L G D L V L T L L L A L A V Y S L G

121/41

151/51

cgc cct gtc tcc cga ggt cta ggt acc gct gaa ggt acc cgt aaa cta ctc att gcc gac  
 R L V S R G Q G T A E G T R K Q H T A E

131/61

211/71

att gag cct ccc ttt ctc gtc ctt ctc ggt ctc aga ctt gag gta ttc agt gtc ttc ttc  
 T E S P Y Q E L L G Q R H E V Y S D L N

241/81

acc cag agt cta ttc ttc aga

T Q R Q Y Y R

Figure 3

ITAM polypeptides	
CD3 $\zeta_1$	YneLnlgrrre-YcrL
CD3 $\zeta_2$	YneLgkckmaaaYseL
CD3 $\zeta_3$	Yqgls tatkat-YdaL
CD3 $\gamma$	Yqplkoreccq-YsnL
CD3 $\delta$	Yqplrcrrccq-YshL
CD3 $\epsilon$	YepLrkqqrnl-YsqL
I $\epsilon\alpha$ (CD79a)	Yedls qglqgt-YqcV
I $\epsilon\beta$ (CD79b)	Yeqldl cqtat-YedL
Fc $\epsilon$ R $\gamma$	Yqplcttrnges-YetL
Fc $\epsilon$ R $\beta$	YeeLmlysat--YsaL
Fc $\epsilon$ R $\alpha$	YqaLqggqrner-YsdL
Consensus	Y--L-----Y--L 

Figure 10A

SEQ ID n°6

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
TCACACGCGG	TTCGACGAGG	CGTCGACGTC	TGGTGTGCGC	TGCATATGTC	50
GGCAGCATCG	GGCTGTGGAG	CGTCTGTGGG	CGTTGTGTTG	CTTCTGTGTC	100
TCTGCACTCT	GGGACGATTA	ACTGCGGTTC	ACGCGGTGAG	TGACGCTTTC	150
CGACGATTCG	ATTGTTGTTG	CGTGCGGCTT	GGTGATCTGT	CTGGGATCTT	200
TCTGGGTGAC	TGGTGTTCGA	CTGTCTGTAT	TGCGCTGGCT	GTGACTCTTC	250
TGGCGCGGCT	GGTGTGCGTA	GGTGACGGA	CGCGGTGAGG	GACCGCGAAA	300
CGACGCTTTC	CTGCGATCTA	GTGCGCTTTC	CGCGGCTTTC	AGGCTGCTTC	350
ACTGCACTTA	TACGTGACCG	TGACGACGCA	CGCGGATTC	TACGATGAG	400
CGGATCTTTC	GGGATCTTTC	GGGATCTTTC	CGCGGCTTTC	TGATCTGAG	450
TCTGCACTTA	AGGCGGCTTC	TGTCGATCTA	CGGATCTTTC	TGCACTTTC	500
ATTGCACTTC	TTCTT				515

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
SHYVRRAPG	ACFVHNEFW	GGGASWGLF	LPVLTUGCL	SPVQACSDTF	50
FRDGSVSP	GVLSGIVLGD	LVTLALALA	VYSLGFLVSR	GGGREGIRK	100
GVPAIESPA	GVLSGQFHEV	YSLNTQFQY	VHGFHEPLS	GVLPGGGSR	150
GVLPFSIRS	GVLPFSIRG	Y			171

Figure 10B

SEQ ID n°11

12.26

Figure 11A

SEQ ID n°7

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
GTGCGCTCTT	GGGCGCGCTG	GGGCGCTCTG	AGCGCGCTCT	GTGCGCTCTG	50
TTGCGCTCTG	TTGCGCTCTG	TTGCGCTCTG	TTGCGCTCTG	TTGCGCTCTG	100
GTGCGCTCTT	GGGCGCGCTG	GGGCGCTCTG	AGCGCGCTCT	GTGCGCTCTG	150
TTGCGCTCTG	TTGCGCTCTG	TTGCGCTCTG	TTGCGCTCTG	TTGCGCTCTG	200
GTGCGCTCTT	GGGCGCGCTG	GGGCGCTCTG	AGCGCGCTCT	GTGCGCTCTG	250
TTGCGCTCTG	TTGCGCTCTG	TTGCGCTCTG	TTGCGCTCTG	TTGCGCTCTG	300
GTGCGCTCTT	GGGCGCGCTG	GGGCGCTCTG	AGCGCGCTCT	GTGCGCTCTG	350
TTGCGCTCTG	TTGCGCTCTG	TTGCGCTCTG	TTGCGCTCTG	TTGCGCTCTG	371

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
ATGCGCTCTT	GGGCGCGCTG	GGGCGCTCTG	AGCGCGCTCT	GTGCGCTCTG	50
TTGCGCTCTG	TTGCGCTCTG	TTGCGCTCTG	TTGCGCTCTG	TTGCGCTCTG	100
GTGCGCTCTT	GGGCGCGCTG	GGGCGCTCTG	AGCGCGCTCT	GTGCGCTCTG	123

Figure 11B

SEQ ID n°12

13 26

Figure 12A

SEQ ID n°8

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
GGCTTCGCTT	CGTTCCTGTC	CTTCCTGACTG	TGGGAGGCTT	AACCTCCGCTA	50
CGAGCCCGCA	GTGAGCTTTT	CCGAGAGTCC	CGCTGTTCTT	CCGTGAGCCC	100
TGCTGACTG	CGTGGGCTG	TTTGGGCTG	CTTGGGCTG	AATCTGCTGA	150
TTGCTTCGGC	TGTGACTCT	CTGGCCCGCC	TGTTTCCCG	AGGTGAGGG	200
AGAGCCGAG	CGAGCCGGA	AGAGAGATT	GTGAGCTG	AATCGCTTA	250
TGAGGCTT	CGGGTCTGA	GAGTGAAT	AGAGCTGAC	CTGAGCTGC	300
AGAGTGAAT	TTAGCTGA	GGCTGCTA	TGGCTGAG	CGGCTGCTG	350
CGGCTGCG	GTGATTCGAG	ATGCTT			376

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
ATGCTTCTT	CGCTGAGCTT	CTTCCTGACTG	TGGGAGGCTT	AACCTCCGCTA	50
AGAGTGAAT	TTAGCTGA	GGCTGCTA	TGGCTGAG	CGGCTGCTG	100
CGGCTGCG	GTGATTCGAG	ATGCTT			124

Figure 12B

SEQ ID n°13

14.2b

SEQ ID n°9

Figure 13A

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
CGAGGCGCGT	GAATGTGCTG	TGCTGTGCTG	AGTGGGCGAC	GTGGGGGGCT	50
GTGGAGCGTG	GTGGTCCGTT	GTGGTCCGTT	GTGGTCCGTT	GTGGTCCGTT	100
GGATTAAGTG	GGATTAAGTG	GGATTAAGTG	GGATTAAGTG	GGATTAAGTG	150
TGTTGCGTGT	AGCGGTGCTG	AGCGGTGCTG	AGCGGTGCTG	AGCGGTGCTG	200
TGTTGCGTGT	AGCGGTGCTG	AGCGGTGCTG	AGCGGTGCTG	AGCGGTGCTG	250
TGTTGCGTGT	AGCGGTGCTG	AGCGGTGCTG	AGCGGTGCTG	AGCGGTGCTG	300
TGTTGCGTGT	AGCGGTGCTG	AGCGGTGCTG	AGCGGTGCTG	AGCGGTGCTG	350
TGTTGCGTGT	AGCGGTGCTG	AGCGGTGCTG	AGCGGTGCTG	AGCGGTGCTG	400
TGTTGCGTGT	AGCGGTGCTG	AGCGGTGCTG	AGCGGTGCTG	AGCGGTGCTG	450

11

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
25LGGGQQCT	SGHGGGGGAS	WGLFLPAA	TGGLSPVQA	QSDTFFPQDC	50
SSVSPGVLAG	TVGLVMTL	LPLVYSLS	PLVSPQQT	EGVFPQFLAE	100
TSPYQELQG	QFFPVYSLS	TSPYQELQG	LSP		150

Figure 13B

SEQ ID n°14

15.20

Figure 14A

SEQ ID n°10

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
CTTCTCTCTCT	GTCTCTCTCTA	CTCTCTCTCTG	ACTCTCTCTCT	CTTCTCTCTCT	50
ACTCTCTCTCT	TTTCTCTCTCT	TCTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	100
CTTCTCTCTCT	TTTCTCTCTCT	TCTCTCTCTCT	TTTCTCTCTCT	TCTCTCTCTCT	150
CTTCTCTCTCT	TCTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	200
CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	250
CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	300
CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	350
CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	400
CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	450
CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	460

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
CTTCTCTCTCT	GTCTCTCTCTA	CTCTCTCTCTG	ACTCTCTCTCT	CTTCTCTCTCT	50
ACTCTCTCTCT	TTTCTCTCTCT	TCTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	100
CTTCTCTCTCT	TTTCTCTCTCT	TCTCTCTCTCT	TTTCTCTCTCT	TCTCTCTCTCT	150
CTTCTCTCTCT	TCTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	CTTCTCTCTCT	160

Figure 14B

SEQ ID n°15





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Figure 15 (contd.)

AA098506	-----	-----	-----	-----	-----	402
AA242315	-----	-----	-----	-----	-----	448
W88159	-----	-----	-----	-----	-----	369
AA734769	-----	-----	-----	-----	-----	371
W41142	-----	-----	-----	-----	-----	362
Consensus	AGGCGACTGT	ATGCGCATCA	GGCGGCTGAT	GGCGGCAATC	GGCAATGCA	450
AA098506	-----	-----	-----	-----	-----	402
AA242315	-----	-----	-----	-----	-----	497
W88159	-----	-----	-----	-----	-----	376
AA734769	-----	-----	-----	-----	-----	371
W41142	-----	-----	-----	-----	-----	412
Consensus	GAAGGCTACT	CAACAAGCCC	TTCTSTGRGA	TCAGGACTCC	CGTGGGACA	500
AA098506	-----	-----	-----	-----	-----	402
AA242315	-----	-----	-----	-----	-----	515
W88159	-----	-----	-----	-----	-----	376
AA734769	-----	-----	-----	-----	-----	371
W41142	-----	-----	-----	-----	-----	462
Consensus	CAGATCCACA	GGTACCTCC	CTGAGATATC	TCAGATGTA	CCATTTCGT	550
AA098506	-----	-----	-----	-----	-----	402
AA242315	-----	-----	-----	-----	-----	515
W88159	-----	-----	-----	-----	-----	376
AA734769	-----	-----	-----	-----	-----	371
W41142	-----	-----	-----	-----	-----	482
Consensus	CCCCAATAG	AAGACCGACA	-----	-----	-----	570



[illegible]

20.26

Figure 17 (contd.)

SEQ ID n° 18 (contd.)

10	20	30	40	50	
1034567890	1034567890	1034567890	1034567890	1034567890	
GGGCTACCA	AACTAACCT	CTCTACAGC	AACTAACCA	ACAAAAACA	2100
AACTAACCA	AACTAACCT	CACTACAGC	CTCTACAGT	CGCTACAGC	2150
CGGCTACCA	TAATTAACA	CACTACAGC	AACTAACCA	AACTAACCA	2200
CTCTACAGT	TAATTAACA	TAATTAACA	GGGCTACCA	TGGCTACCA	2250
CACTACAGC	AACTAACCA	CTCTACAGC	CGCTACAGC	AACTAACCA	2300
GGGCTACCA	TAATTAACA	TAATTAACA	CGCTACAGC	CGCTACAGC	2350
CACTACAGC	AACTAACCA	AACTAACCA	AACTAACCA	CTCTACAGC	2400
GGGCTACCA	AACTAACCA	GGGCTACCA	TGGCTACCA	GGGCTACCA	2450
CTCTACAGT	TAATTAACA	GGGCTACCA	CTCTACAGC	AGGCTACCA	2500
GGGCTACCA	TGGCTACCA	AACTAACCA	AACTAACCA	TTTCTACCA	2550
TTTCTACCA	AACTAACCA	CACTACAGC	CACTACAGC	AACTAACCA	2600
AACTAACCA	AACTAACCA	GGGCTACCA	TGGCTACCA	TTTCTACCA	2650
TTTCTACCA	TGGCTACCA	CACTACAGC	CACTACAGC	AACTAACCA	2700
AACTAACCA	TAATTAACA	CACTACAGC	TGGCTACCA	AACTAACCA	2750
TGGCTACCA	GGGCTACCA	AACTAACCA	TGGCTACCA	CTCTACAGC	2800
TGGCTACCA	GGGCTACCA	CACTACAGC	GGGCTACCA		2850

21.2b

Figure 133' Intron sequence  
(donor site)

Exon sequence

5' Intron sequence  
(acceptor site)MetGly                      21G12G  
ATGCGG...-Exon 1-...TCCAGG

GAGGTGA....

....TCCTTAC

IyLeuS                      1nS9rA  
GATTAA...-Exon 2-...ACAGTG

GTAAGCC....

....TCCTCAG

spThrP                      1nG12A  
ACACTT...-Exon 3-...AACAGA

GTAAGAA....

....TCTCTAG

rgThcA                      TyeGln  
GGACCC...-Exon 4-...TATCAG

GTAAGAA....

....TTTAAAG

Figure 2

22.26

	10	20	30	40	50	
	103456789	103456789	103456789	103456789	103456789	
SEQ ID n <sup>o</sup> 21	ATGGGGGGCTT	TGGAGCCCTC	CTGGTGGCTT	CTCTTGGCTT	CTGTGCTGCT	50
SEQ ID n <sup>o</sup> 23	M G A L E P S	N C L L F L P	V L L			
	GACTGTGGAC	GCATTAAGTC	CCCTACACGC	CCAGGTGAC	ACTTTCCCAA	100
	T V E G L S P	V Q A Q S D	T F P R			
	GATGGGACTC	TTCTTGGCTC	AGCCCTGGTG	TACTGGCTGC	CAATCTTCTC	150
	C D C S S V	S P G V L A G	I V L			
	CGTGGCTTGG	TCTTCACTCT	CGTCATTGCC	CTGGCTGTCT	ACTCTCTGGG	200
	G D L V L T L	L E A L A V Y	E L S			
	CGCCCTGGTC	TCCCGAGGTC	AACACAGGAC	CGGCAACAA	CACATTGCTC	250
	R L V S R G Q	E R T R K Q	H I A E			
	AGACTGAGTC	GCCTTATCAG	CAGTTTCAGG	CTCAGACACA	TGAAGTATAC	300
	T E S P Y Q	E L Q G Q R H	E V Y			
	AGTGCCTCA	ACACACAGAG	GCAATATTAC	AGATGAGCCG	ACTCTATGCC	350
	S D L N T Q R	Q Y Y R A H	S M P			
	CATCAGCCGC	CTGATGCCCG	GATCCGGTCA	TTCAGATCC	CTACTCAACA	400
	I S G L M P G	S G H S R C	L L N K			
	AGCCCTCTCT	GAGATCAGGA	CTCCCGTTGG	AATACAGATC	CACAGGGTAC	450
	P S L R S G	L P L E Y R S	T G Y			
CT						452

23.26

Figure 20

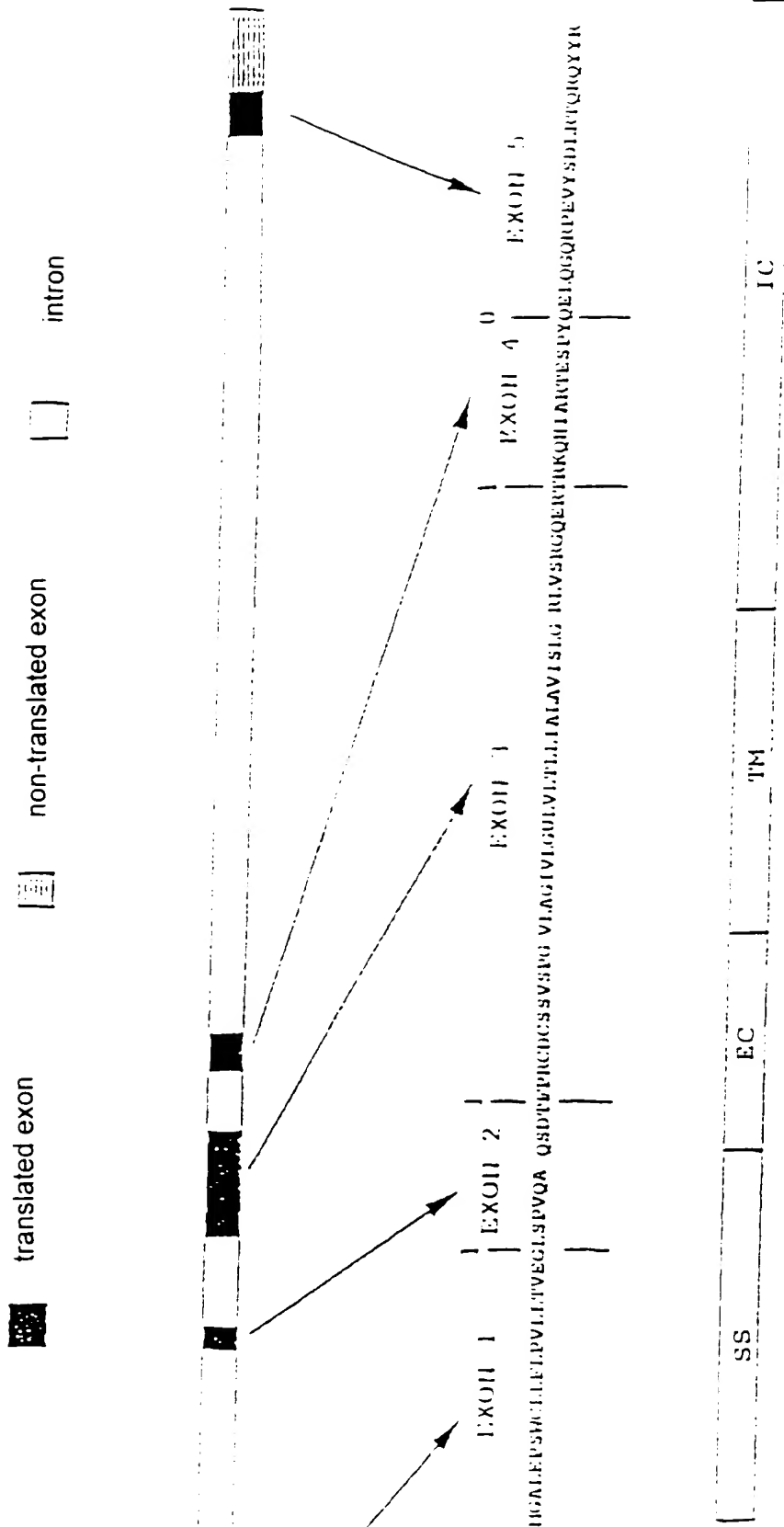






Figure 22

Release of serotonin induced by the p50/KARAP  
complex reconstituted in RBL-2H3 cells

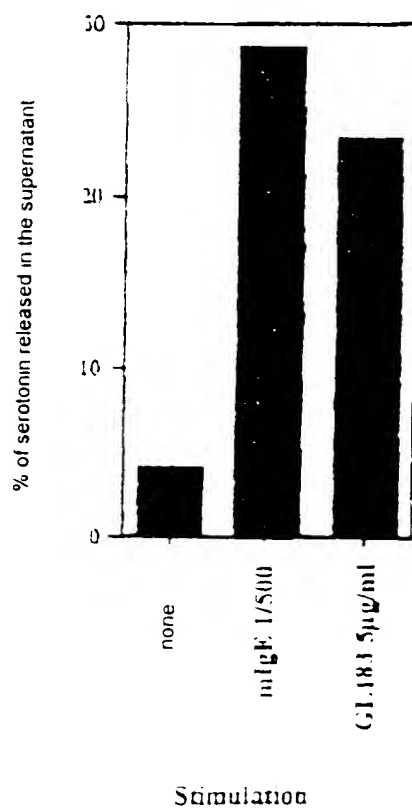


Figure 23

